Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:42:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013183.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:42:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,104,151
Mapped reads	1,521,229 / 72.3%
Unmapped reads	582,922 / 27.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,817 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	161,815 / 7.69%
Duplication rate	8.78%
Clipped reads	1,133,680 / 53.88%

2.2. ACGT Content

Number/percentage of A's	26,016,484 / 29.04%
Number/percentage of C's	16,833,830 / 18.79%
Number/percentage of T's	27,433,266 / 30.63%
Number/percentage of G's	19,289,504 / 21.53%
Number/percentage of N's	727 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2947

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

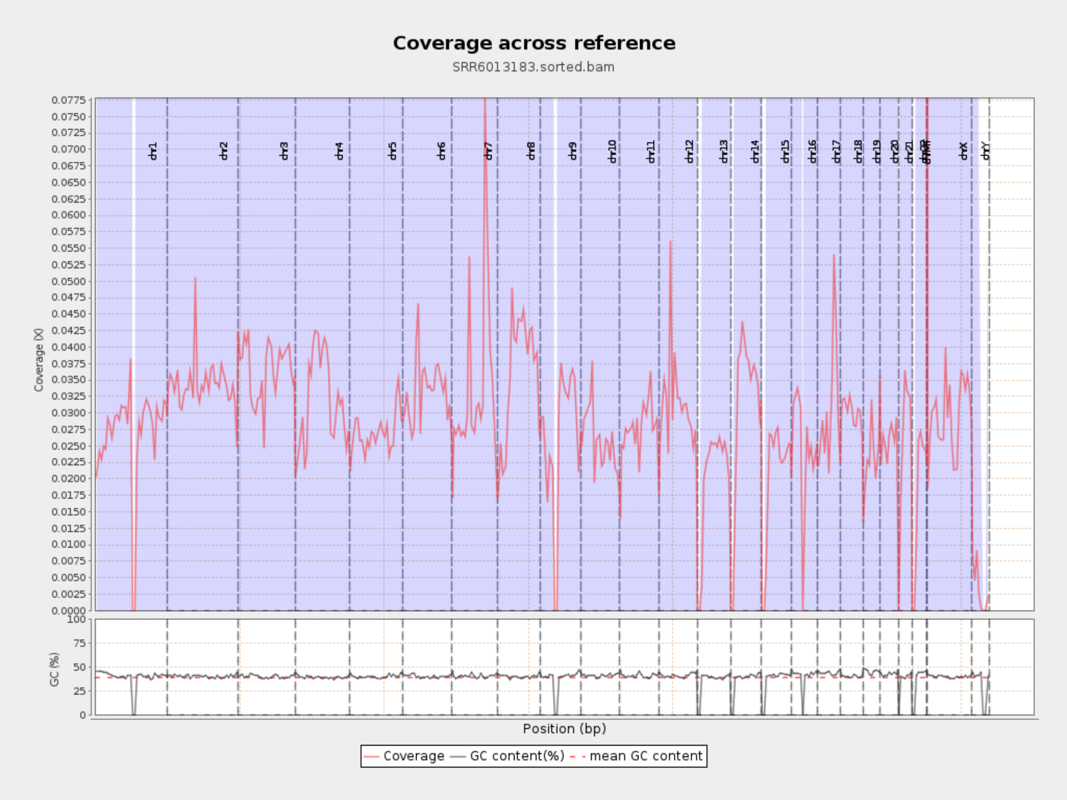
General error rate	0.84%
Mismatches	743,674
Insertions	6,284
Mapped reads with at least one insertion	0.41%
Deletions	24,636
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.42%

2.6. Chromosome stats

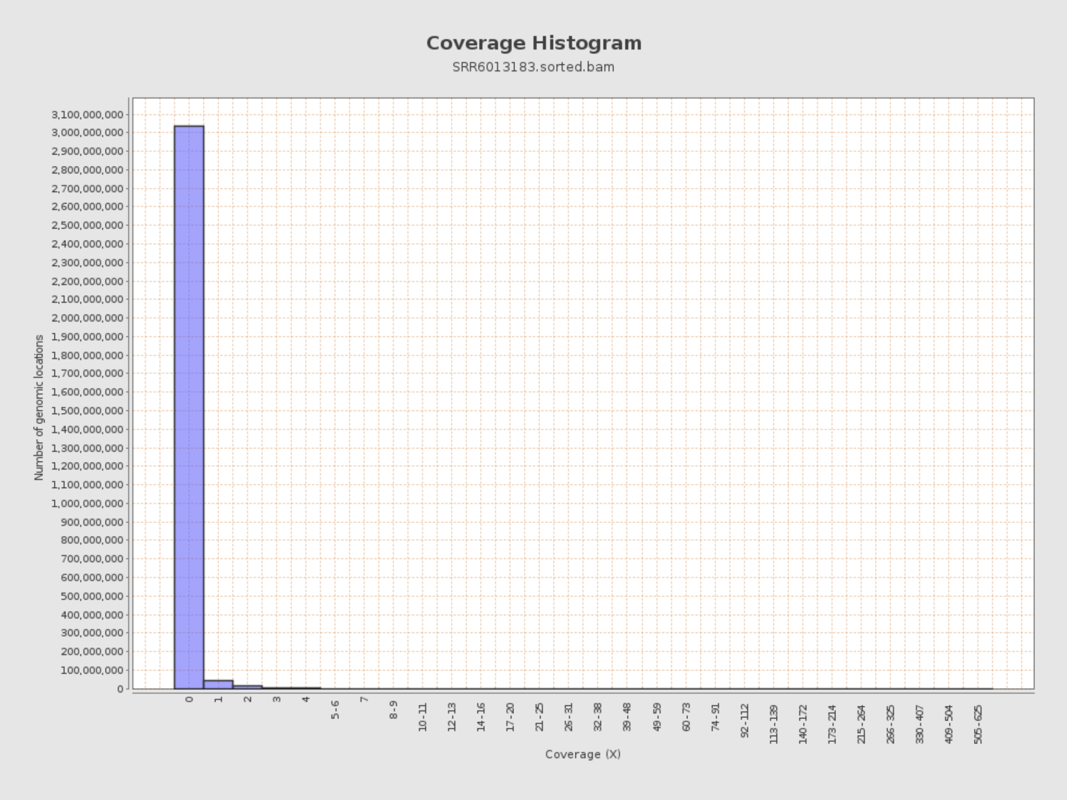
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6652661	0.0267	0.3494
chr2	243199373	8351603	0.0343	0.3651
chr3	198022430	7240799	0.0366	0.2614
chr4	191154276	6105069	0.0319	0.2524
chr5	180915260	4903314	0.0271	0.2268
chr6	171115067	5717381	0.0334	0.2841
chr7	159138663	5382934	0.0338	0.4648

chr8	146364022	5302226	0.0362	0.4404
chr9	141213431	3693846	0.0262	0.2619
chr10	135534747	3509910	0.0259	0.2744
chr11	135006516	3759771	0.0278	0.2569
chr12	133851895	4214456	0.0315	0.2441
chr13	115169878	2283390	0.0198	0.1919
chr14	107349540	3328693	0.031	0.2463
chr15	102531392	2080207	0.0203	0.2022
chr16	90354753	2167934	0.024	0.2127
chr17	81195210	2499157	0.0308	0.2463
chr18	78077248	2363480	0.0303	0.3804
chr19	59128983	1402700	0.0237	0.2871
chr20	63025520	1600159	0.0254	0.222
chr21	48129895	1259727	0.0262	0.2244
chr22	51304566	912140	0.0178	0.1752
chrMT	16571	59409	3.5851	3.5067
chrX	155270560	4633025	0.0298	0.2488
chrY	59373566	190629	0.0032	0.0783

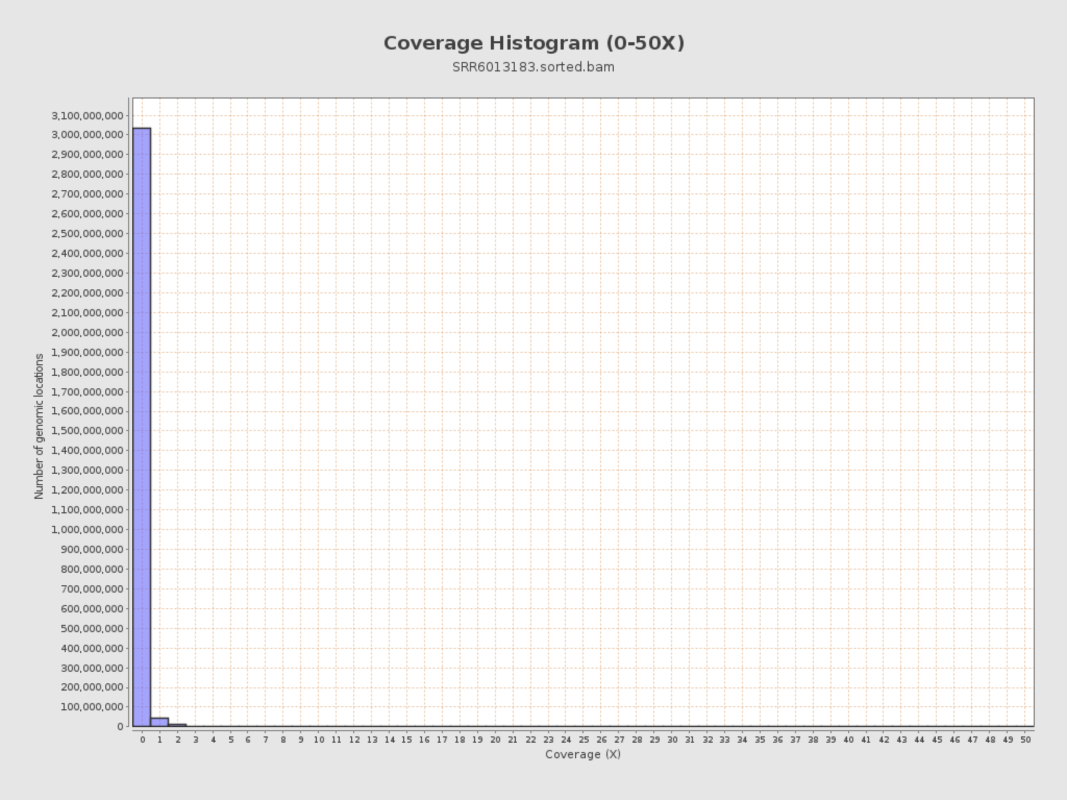
3. Results : Coverage across reference



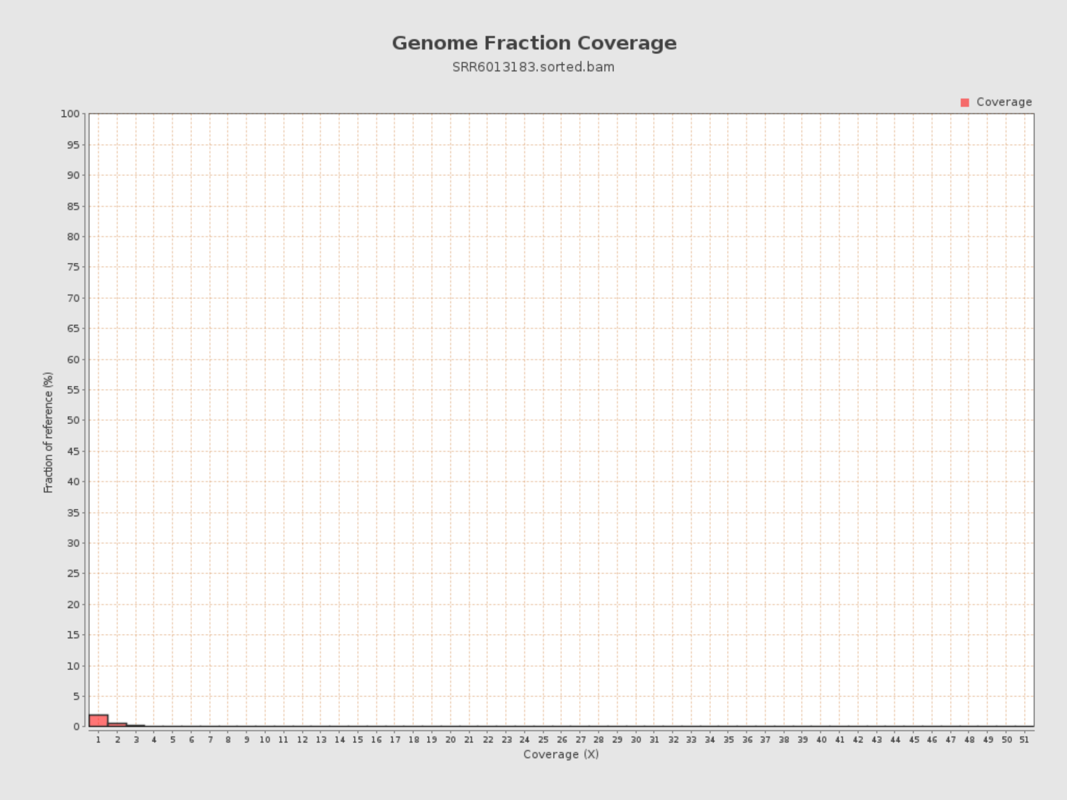
4. Results : Coverage Histogram



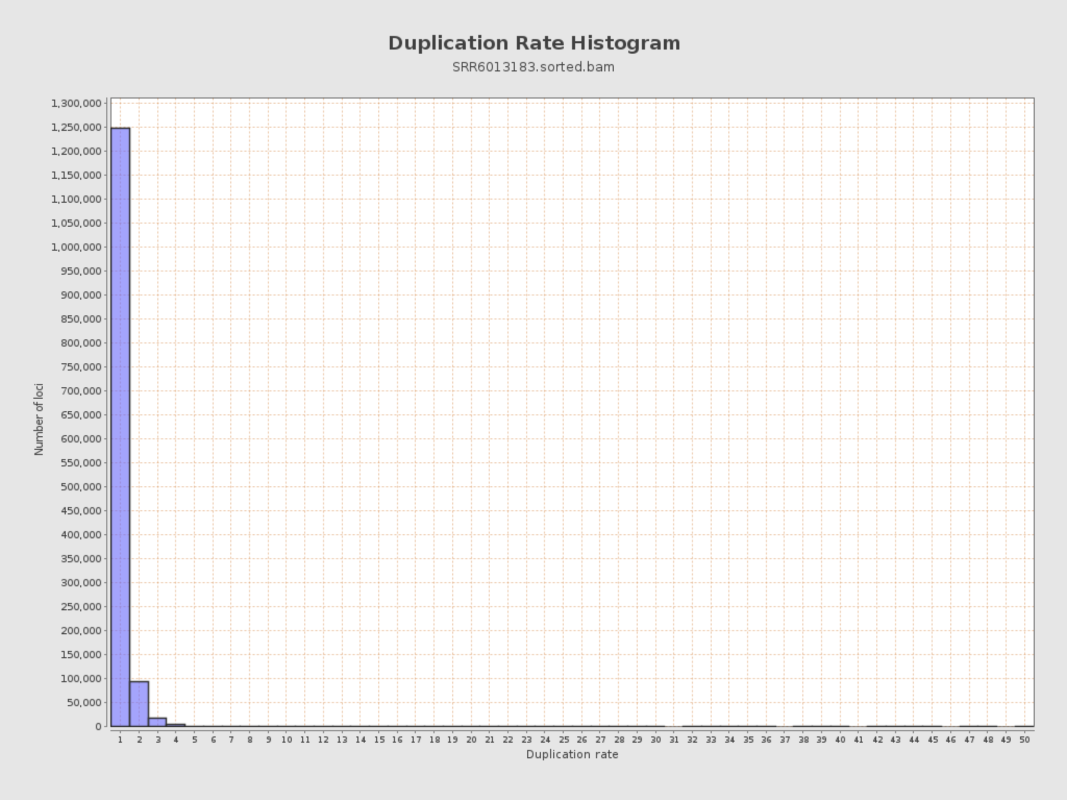
5. Results : Coverage Histogram (0-50X)



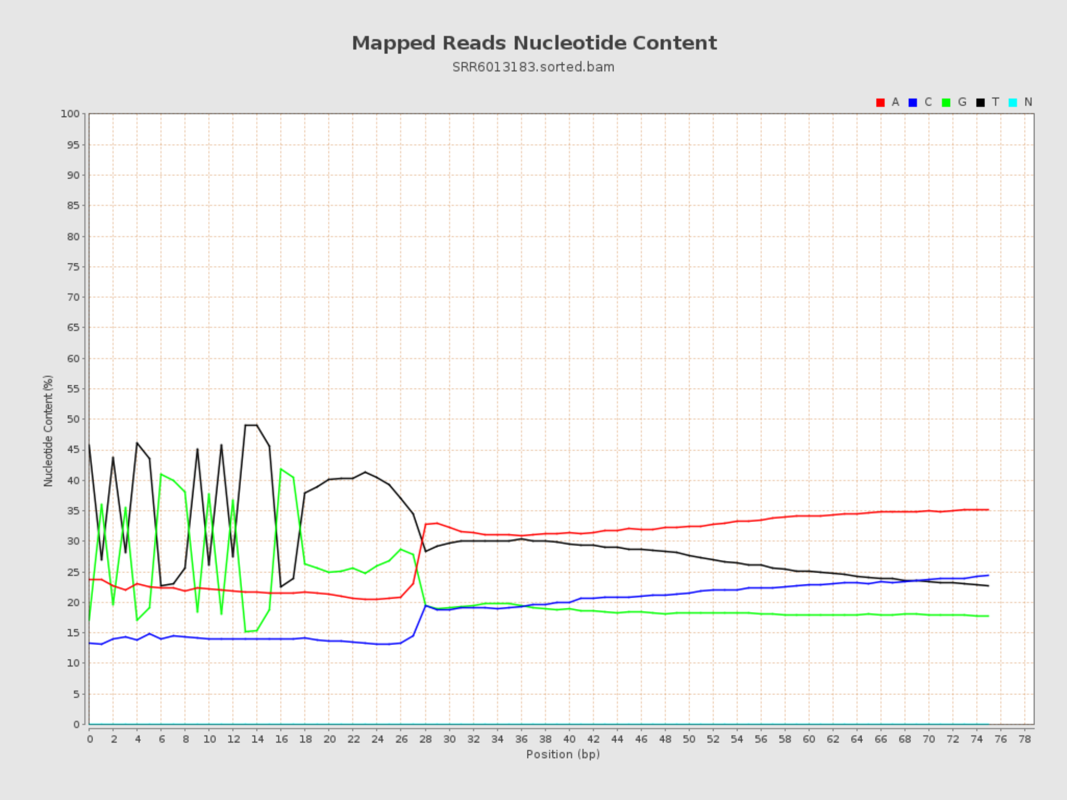
6. Results : Genome Fraction Coverage



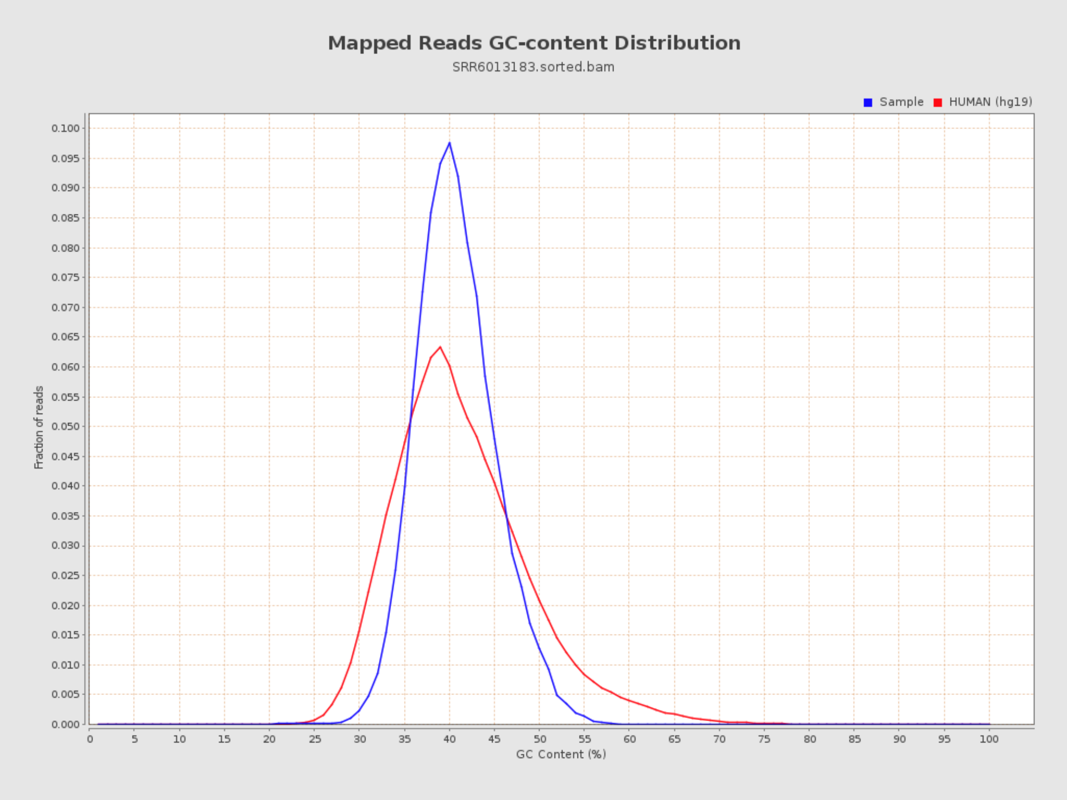
7. Results : Duplication Rate Histogram



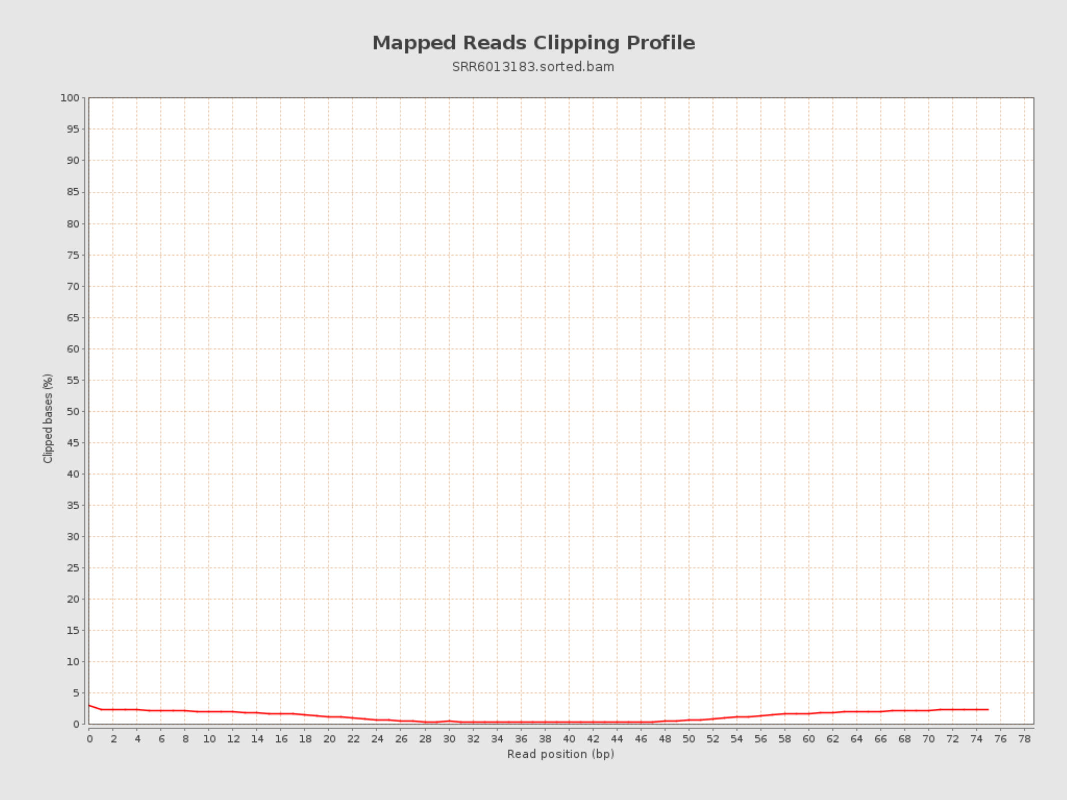
8. Results : Mapped Reads Nucleotide Content



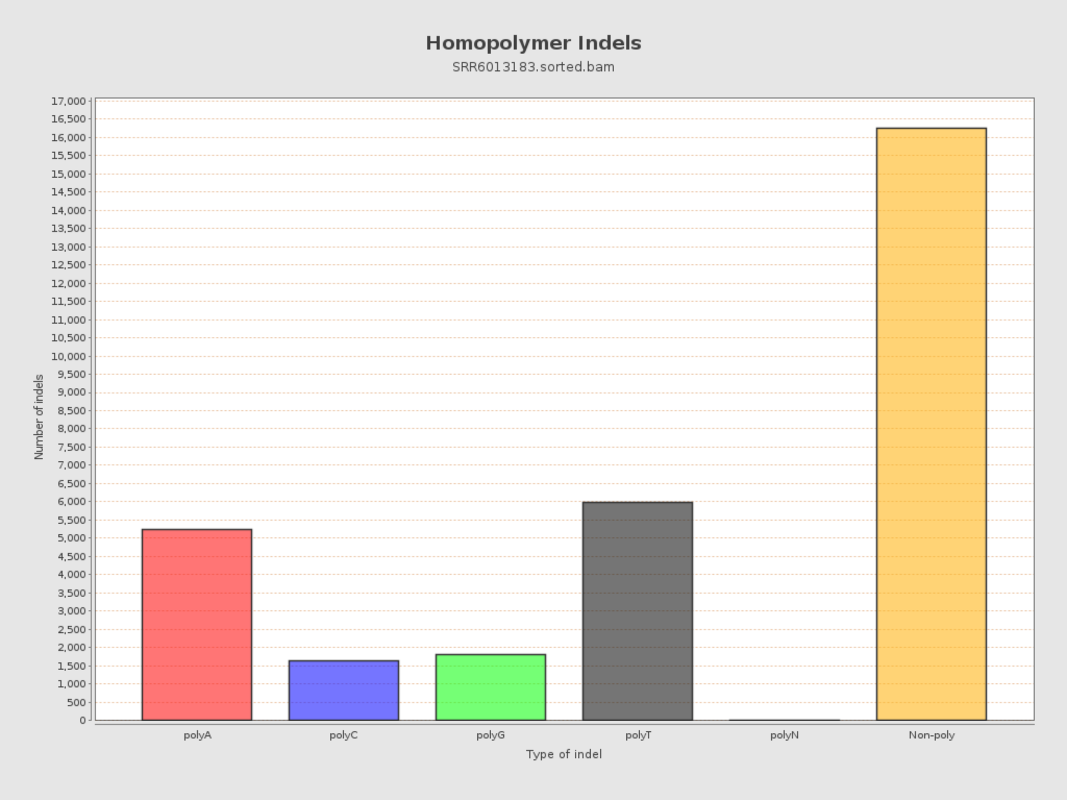
9. Results : Mapped Reads GC-content Distribution



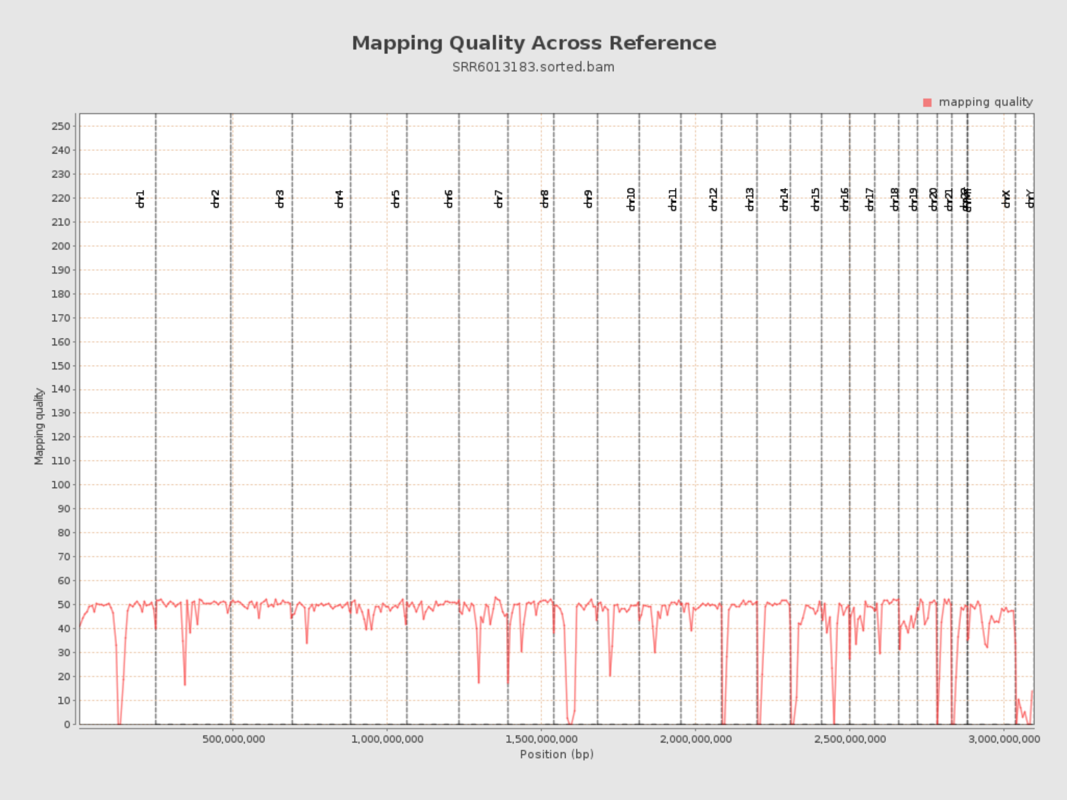
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram